

AMENDMENTS TO THE DRAWINGS

The attached replacement sheet of drawings includes a change to Figure 2. In Figure 2, the url is deleted, as requested in the Office Action. The replacement sheet replaces the original sheet for Figure 2.

Attachments: Replacement Sheet

Annotated Sheet showing changes

REMARKS

Claims 1-19 are pending in the present Application, with claims 10-18 withdrawn from consideration as directed to nonelected subject matter. Thus, claims 1-9 and 19 are under consideration.

Claims 1-9 and 19 are amended. No new matter has been introduced by these amendments as antecedent basis for these amendments is found at least at p. 2, lines 9-12; p. 3, lines 3-4; p. 5, lines 10-13; p. 6, lines 3-5; p. 7, lines 18-19; Table 1 (p. 5); Fig. 4; and claim 3 as originally filed.

Reconsideration and allowance of the claims are respectfully requested in view of the above amendments and the following remarks.

Interview of January 25, 2007

Applicants thanks the Examiner for the courtesy of a phone interview with Applicants' agent on January 25, 2007 to discuss the §101 and §112, 2nd paragraph rejections. Possible claim amendments to overcome these rejections were discussed.

Objections to the Drawings

Figures 2 and 3 were objected to because each had sequence disclosures requiring submission of a sequence listing in compliance with the requirements of 37 CFR § 1.821 through 1.825. Submitted herewith is a sequence listing in compliance with the requirements and a statement under 37 CFR § 1.821(f) and (g). Applicants request entry of the sequence listing into the application. Further, Applicants have amended the BRIEF DESCRIPTION OF THE DRAWINGS for figures 2 and 3 to include references to the sequence identification numbers used in the attached sequence listing.

Figure 2 was additionally objected to for including an embedded hyperlink. A replacement Fig. 2 is attached in which the embedded hyperlink is deleted.

Applicants believe that the drawings are now fully compliant with all rules and request reconsideration and withdrawal of the objections to the drawings.

Claim Objections

Claim 2 was objected to because of a grammatical informality. The claim is amended to have the noun and verb agree in form. Applicants request reconsideration and withdrawal of this objection to claim 2.

Claim Rejections Under 35 U.S.C. § 101

Claims 1-2, 4-9, and 19 stand rejected under 35 U.S.C. § 101 as directed to nonstatutory subject matter. Applicants respectfully traverse this rejection.

The Examiner stated that a statutory process must include a step of a physical transformation, or produce a useful, concrete, and tangible result, and that the instant claims fail to do so.

Applicants assert that Claim 1, as originally filed, is directed to statutory subject matter. 35 U.S.C. 101 reads: “Whoever invents or discovers any new and useful process, **machine**, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title” (emphasis added). Claim 1, as originally filed, is directed to an apparatus (i.e., a machine) which performs a highly practical function, encoding a DNA sequence to achieve a high data compression ratio for storage or transfer. As such, Claim 1, and dependent claims 2, 4-9, are directed to the statutory class of a “machine” and are believed to be fully compliant with the requirements set forth in 35 U.S.C. 101.

However, although Applicants disagree with the interpretation of the Interim Guidelines for Subject Matter Eligibility that to demonstrate that an apparatus can perform a tangible result requires an explicit statement that it communicates to the outside world, to further prosecution, Applicants have amended claim 1 to incorporate a limitation of claim 3, as originally filed, that the conversion unit is for outputting the string of characters. Thus claims 1, 2, 4-9 are fully compliant with 35 U.S.C. 101, as well as the Interim Guidelines.

Furthermore, with respect to the rejection of claim 19, Applicants have amended claim 19 to state that the computer readable medium is not a carrier wave.

Applicants request reconsideration and withdrawal of the rejections of claims 1, 2, 4-9 and 19 under 35 U.S.C. 101.

Claim Rejections Under 35 U.S.C. § 112, Second Paragraph

Claims 1-9 and 19 stand rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. In particular, the Examiner has stated that the phrase “the individual character” as recited in claims 1 (p. 16, line 10) and 19 (p. 19, line 19) lacks antecedent basis. Claims 2-9 are indefinite due to their dependency from claim 1. In addition, the Examiner has stated that the phrase “the character” as recited in claims 1 (p. 16, line 11), 2 (p. 16, line 14), 5 (p. 17, line 2), 6 (p. 17, line 7) and 19 (p. 19, line 19) lacks antecedent basis. Claims 3-4 and 7-9 are also rejected due to their dependency from claim 1. Also, the phrase “the various sequence induction factor” as recited in claim 9 (p. 17, line 18) lacks antecedent basis. Further, the Examiner has stated that the meaning of the phrase “continuation of the difference” in claim 2 (p. 16, line 17) is unclear. Claim 3 is rejected due to its dependency from claim 2. The Examiner has also stated that the meanings of the phrases “starting, ... and outputs the string of the characters.” (p. 16, lines 20-24) as recited in claim 3 are unclear. Additionally, the Examiner has stated that it is unclear whether all or just one of the listed limitations in claim 4 need to be present to be considered the “difference.” Lastly, the Examiner has stated that the meanings of the phrases “blank by base deletion” and “variation sequence generation factor” as recited in claims 4 and 8 respectively are unclear.

The language of the claims has been amended to more particularly point out the claimed invention. Applicants believe that the amendments overcome all of the above issues.

Applicants therefore request reconsideration and withdrawal of the rejection of claims 1-9 and 19 under 35 U.S.C. § 112, second paragraph.

Claim Rejections Under 35 U.S.C. § 102(b)

Claims 1, 6, 7 and 19 stand rejected under 35 U.S.C. § 102(b), as allegedly anticipated by Grumbach et al. (Information, Processing & Management, Volume 30, Number 6, pages 875-886, 1994). Applicants respectfully traverse this rejection.

To anticipate a claim, a reference must disclose each and every element of the claim. *Lewmar Marine v. Variant Inc.*, 3 U.S.P.Q.2d 1766 (Fed. Cir. 1987).

Grumbach et al. generally disclose the somewhat unique challenges associated with

compression of nucleic acid sequences. In particular, Grumbach et al. briefly discuss classical compression algorithms and their failure to provide satisfactory compression of nucleic acid sequences, and then present the biocompress-2 algorithm for compression of a nucleic acid sequence by using sequence regularities, such as palindromes. (abstract)

The Examiner alleged that Grumbach et al. disclose using UNIX, a computer operating system, to encode DNA sequences which represents the apparatus of independent claim 1 and ASCII files with algorithms to encode DNA which represents the computer readable medium of independent claim 19.

Applicants disagree with these allegations. Applicants note that UNIX is a computer operating system, and although in the 2nd paragraph of p. 876, cited by the Examiner as a disclosure of “using UNIX”, lines 1-2 state Grumbach et al. applied two algorithms *from* Unix on samples of DNA and RNA sequences, nowhere is there disclosure that the apparatus performing either algorithm comprises a comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence; a conversion unit for converting the extracted difference between the reference sequence and the subject sequence into a string of characters and for outputting the string of characters; a code storage unit for storing a conversion code that corresponds to a character to represent the extracted difference; and an encoding unit for encoding the string using the conversion code. In particular, Grumbach et al. fail to disclose explicitly in this putative apparatus comprising UNIX the presence of at least a comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence.

The Examiner alleges that the comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence is disclosed by Grumbach et al. however the office action fails to clearly indicate where or how this is disclosed. The Examiner at best stated on p. 8 of the Office Action “Grumbach et al. disclose having a start position and matching the factor at the current position followed by outputting a codeword (p. 881, 2nd para), compression algorithms including a vertical mode, where a DNA sequence A is compressed with respect to another sequence B with output containing information to construct sequence A from sequence B

(p.876, 5th para), using codewords to encode strings and arithmetic encoding (p.876, 3rd para and p. 879, 1st para), and storing a reference sequence in a database while other sequences are stored in a compressed form with respect to it (p.876, 5th para) which represents the comparative, conversion, code storage and encoding units (as stated in instant claim 1), the compression and storage units (as stated in instant claim 7), and the aligning, extracting, converting, and encoding steps (as stated in instant claim 19).” From this sentence, it is truly hard to understand the argument being constructed in the Office Action. Nowhere in any of these cited sections of Grumbach et al. do Applicants see disclosure of at least “aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence” or of “a comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence”.

With respect to the cited section at p. 881, 2nd para., the Biocompress-2 algorithm disclosed on p. 881 is discussed in relationship to compression of a *single* sequence, not for compression of a subject sequence based on extracted differences between a reference sequence and the subject sequence. Also, the Biocompress-2 algorithm is not one of the two compression algorithms available on UNIX (see p. 878, lines 2-3 of “3. Classical Algorithms”) and therefore is apparently NOT part of the “apparatus” that the Examiner alleged is disclosed. Biocompress-2 is disclosed to be based on the “detection and encoding of factors and palindromes” (p. 876, 3rd para), not on converting an extracted difference between a reference sequence and a subject sequence into a string of characters as performed by the conversion unit of claim 1.

With respect to the section cited on p. 876, 5th para, disclosing compression algorithms including a vertical mode in which a DNA sequence A is compressed with respect to another sequence B, there is no disclosure of how the vertical mode performs this compression. In particular, there is no disclosure that this vertical mode performs this compression by “aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence”. Moreover, the paragraph further states that the output of biocompress-2 contains the information to construct the sequence A from sequence B, but as noted above the Biocompress-2 algorithm is not one of the two compression algorithms available on UNIX (see p. 878, lines 2-3 of “3.

Classical Algorithms”) and therefore is apparently NOT part of the “apparatus” that the Examiner alleged is disclosed.

With respect to the section cited on p. 876, 5th para., disclosing “storing a reference sequence in a database while other sequences are stored in a compressed form with respect to it”, this is the only “storing” function noted by the Examiner. A database with a stored reference sequence and with other sequences stored in compressed form relative to the reference is not equivalent to the recited element, “a code storage unit for storing a conversion code that corresponds to a character to represent the extracted difference”. Further, although Grumbach et al. mention use of a dictionary at p. 879, 3rd para.), Applicants cannot find in that paragraph any disclosure that the dictionary is for storing a conversion code that corresponds to a character to represent the extracted difference as required by claim 1.

Thus claim 1 cannot be anticipated by Grumbach et al., as the cited reference fails to disclose each and every element of the claim. As claims 6 and 7 depend from claim 1, they also are not anticipated by Grumbach et al.

More particularly with respect to claim 6, Applicants note that claim 6 requires a division unit for dividing the extracted difference into segments of a predetermined size, and wherein the conversion unit converts the extracted difference into the string which is made up of the characters to represent the extracted difference based on the segments. Grumbach et al. are silent with respect to an “extracted difference” between a reference sequence and a subject sequence, consequently, Grumbach et al. fail to disclose a division unit as required by claim 6 and therefore fail to anticipate claim 6.

With respect to claim 19, Grumbach et al. disclose an invention that compresses DNA sequences using the regularities (palindromes), which exist in the DNA sequences, the present invention converts the extracted difference between the reference sequence and the subject sequence into a string. Applicants can find no place in Grumbach et al. teaching “aligning a reference sequence having known DNA information with a subject sequence to be encoded”, “extracting a difference between the reference sequence and the subject sequence”, or “converting the extracted difference between the reference sequence and the subject sequence into a string of characters” as recited in claim 19. Furthermore, the “ASCII files with algorithms to encode DNA” on p. 878, 2nd and 3rd para. alleged by the Examiner to represent the computer

readable medium of independent claim 19 do not have “algorithms” to encode DNA. As stated in the 2nd sentence of the 3rd para, the ASCII file is a storage form for a DNA sequence, it is not a storage form for a computer program for a method for encoding DNA. Grumbach et al. cannot anticipate claim 19, as they fail to teach each element of the claim.

For at least the above reasons, Applicants respectfully request reconsideration and withdrawal of the rejection of claims 1, 6, 7 and 19 rejected under 35 U.S.C. § 102(b), as allegedly anticipated by Grumbach et al.

Claim Rejections Under 35 U.S.C. § 103(a)

Claims 2-5 stand rejected under 35 U.S.C. § 103(a), as allegedly unpatentable over Grumbach et al. (Information, Processing & Management, Volume 30, Number 6, pages 875-886, 1994) in view of Robson et al. (1992). Applicants respectfully traverse this rejection.

For an obviousness rejection to be proper, the Examiner must meet the burden of establishing a *prima facie* case of obviousness, i.e., that all elements of the invention are disclosed in the prior art; that the prior art relied upon, coupled with knowledge generally available in the art at the time of the invention, contain some suggestion or incentive that would have motivated the skilled artisan to modify a reference or combined references; and that the proposed modification of the prior art had a reasonable expectation of success, determined from the vantage point of the skilled artisan at the time the invention was made.

Robson et al. is generally directed to natural sequence code representations for compression and rapid searching of large (human genome-style) databases of gene or protein sequences (abstract).

The Examiner has stated that Robson et al. supplies the missing elements as required in claims 2-5 that are not disclosed in Grumbach et al. In particular, Robson et al. teach storing and analyzing nucleic acid sequences including using code to signify differences and their number (e.g. blanks, deletions) as required in claims 2 and 4, using 4 bit code as required in claim 5, and using 4 bit codes corresponding to characters including the start or end of the sequence, continue to read, ending, sequence separator, matches, and various other characters as required in claim 3.

However, as noted above in traversing the §102 rejection of claim 1 as anticipated by Grumbach et al., Applicants assert there are additional elements of claim 1 that are not disclosed

by Grumbach et al. that must be taught by Robson et al. for a *prima facie* case of obviousness to be proper. Namely, Robson et al. must also teach at least a comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence and a code storage unit for storing a conversion code that corresponds to a character to represent the extracted difference. Applicants can find no teaching in Robson of at least a “comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence”. Robson et al. do teach the BLAST algorithm for sequence searching, however they do not teach or suggest aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence. Therefore, claim 1 is not obvious over Grumbach et al. and Robson et al. as all elements of the claim are not taught or suggested by the combination.

Further, with respect to claim 2, Robson et al. are silent with respect to “a character representing whether a type of extracted difference occurs in succession in the subject sequence”.

With respect to claim 3, Robson et al. are silent with respect to extracted differences, therefore they do not teach or suggest starting of the extracted difference, a start position of the extracted difference, whether a type of extracted difference occurs in succession in the subject sequence, a number of continued bases in the extracted difference, a base which the extracted difference comprises, ending of the extracted difference, and a distance between the start position and the end position of the extracted difference.

With respect to claim 4, Robson et al are silent with respect to types of extracted differences.

With respect to claim 5, although Robson et al describe 4 bit codes, Robson et al are silent with respect to 4 bit codes to represent a conversion code as required by claim 1, i.e., “a conversion code that corresponds to a character to represent the extracted difference”

Additionally, Applicants could not determine that the string of characters in Grumbach et al. represents the extracted difference between a reference sequence and a subject sequence. Applicants think that the reference sequence, which has already known DNA information, is not the sequence for comparing with the subject sequence in Robson et al., contrary to the assertions

of the Examiner. Furthermore, Applicants could not find a method for constituting the string to represent the extracted difference between the reference sequence and the object sequence as disclosed in the present invention in Robson et al..

Additionally, the present invention has the surprising effect of compressing the subject sequence efficiently by converting the extracted difference into a string and encoding the string.

For all the above reasons, Applicants assert that claims 2-5 are not *prima facie* obvious over Grumbach et al. in view of Robson et al. Applicants request reconsideration and withdrawal of the rejection of these claims.

Claims 8-9 stand rejected under 35 U.S.C. § 103(a), as allegedly unpatentable over Grumbach et al. (Information, Processing & Management, Volume 30, Number 6, pages 875-886, 1994) in view of Selifonov et al. (US 2002/0183934 A1). Applicants respectfully traverse this rejection.

Selifonov et al. is generally directed to “in silico” nucleic acid recombination methods and related integrated systems using genetic operators and libraries made by the in silico recombination methods.

The Examiner has stated that Selifonov et al. supply the missing elements as required in claims 8-9 that are not taught by Grumbach et al. In particular, the Examiner stated that Selifonov et al. teach generating random variation of sequences via multiplication factors as required in claim 8 (See, paragraphs 0075, 0117 and 0197), and variation sequence induction factor (paragraphs 0026-0028) as required in claim 9.

However, as noted above in traversing the §102 rejection of claim 1 as anticipated by Grumbach et al., Applicants assert there are additional elements of claim 1 that are not disclosed by Grumbach et al. that must be taught by Selifonov et al. for a *prima facie* case of obviousness to be proper. Namely, Selifonov et al. must also teach at least a comparative unit for aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence and a code storage unit for storing a conversion code that corresponds to a character to represent the extracted difference.

Applicants can find no teaching in Selifonov of at least a “comparative unit for aligning a

reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence”.

Therefore, claim 1 is not obvious over Grumbach et al. and Selifonov et al. as all elements of the claim are not taught or suggested by the combination and dependent claims 8-9 can therefore also not be obvious over the the combination.

Applicants request reconsideration and withdrawal of the obviousness rejection of claims 8-9.

It is believed that the foregoing amendments and remarks fully comply with the Office Action and that the claims herein should now be allowable to Applicants. Accordingly, reconsideration and allowance are requested.

If there are any additional charges with respect to this Amendment or otherwise, please charge them to Deposit Account No. 06-1130.

Respectfully submitted,

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